

#2



OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/992,964

DATE: 01/28/2002

TIME: 16:42:21

Input Set : N:\Crf3\RULE60\09992964.raw

Output Set: N:\CRF3\01282002\I992964.raw

ENTERED

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1 <110> APPLICANT: Ashkenazi, Avi J.
2   Baker, Kevin
3   Gurney, Austin
4   Wood, William
5 <120> TITLE OF INVENTION: Apo-2DcR
6 <130> FILE REFERENCE: P1110
8 <140> CURRENT APPLICATION NUMBER: 09/992,964
9 <141> CURRENT FILING DATE: 2001-11-19
11 <150> PRIOR APPLICATION NUMBER: 08/878,168
12 <151> PRIOR FILING DATE: 1997-06-18
15 <160> NUMBER OF SEQ ID NOS: 17
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 259
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
21 <400> SEQUENCE: 1
22   Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
23       1           5           10           15
24   Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
25               20           25           30
26   Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
27               35           40           45
28   His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
29               50           55           60
30   Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
31               65           70           75
32   Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
33               80           85           90
34   Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
35               95          100          105
36   Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
37               110          115          120
38   Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
39               125          130          135
40   Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val
41               140          145          150
42   Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu
43               155          160          165
44   Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
45               170          175          180
46   Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
47               185          190          195
48   Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu

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49          200          205          210
50      Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
51          215          220          225
52      Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
53          230          235          240
54      Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
55          245          250          255
56      Ile Val Phe Val
57          259
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 1180
61 <212> TYPE: DNA
62 <213> ORGANISM: Homo sapiens
63 <220> FEATURE:
64 <221> NAME/KEY: CDS
65 <222> LOCATION: (193) . . . (969)
66 <223> OTHER INFORMATION:
67 <400> SEQUENCE: 2
68      gctgtgggaa cctctccacg cgcacgaact cagccaacga tttctgatag 50
69      atttttggga gtttgaccag agatgcaagg ggtgaaggag cgcttcctac 100
70      cgttagggaa ctctggggac agagcgcccc ggccgcctga tggccgagggc 150
71      aggggtgcgac ccaggaccca ggacggcgctc gggaaccata cc atg 195
72                                     Met
73                                     1
74      gcc cgg atc ccc aag acc cta aag ttc gtc gtc gtc atc 234
75      Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile
76          5          10
77      gtc gcg gtc ctg ctg cca gtc cta gct tac tct gcc acc 273
78      Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr
79      15          20          25
80      act gcc cgg cag gag gaa gtt ccc cag cag aca gtg gcc 312
81      Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
82          30          35          40
83      cca cag caa cag agg cac agc ttc aag ggg gag gag tgt 351
84      Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys
85          45          50
86      cca gca gga tct cat aga tca gaa cat act gga gcc tgt 390
87      Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys
88          55          60          65
89      aac ccg tgc aca gag ggt gtg gat tac acc aac gct tcc 429
90      Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
91          70          75
92      aac aat gaa cct tct tgc ttc cca tgt aca gtt tgt aaa 468
93      Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys
94      80          85          90
95      tca gat caa aaa cat aaa agt tcc tgc acc atg acc aga 507
96      Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
97          95          100          105
98      gac aca gtg tgt cag tgt aaa gaa ggc acc ttc cgg aat 546

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## RAW SEQUENCE LISTING

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Input Set : N:\Crif3\RULE60\09992964.raw

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99      Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn
100      110      115
101      gaa aac tcc cca gag atg tgc cgg aag tgt agc agg tgc 585
102      Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys
103      120      125      130
104      cct agt ggg gaa gtc caa gtc agt aat tgt acg tcc tgg 624
105      Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
106      135      140
107      gat gat atc cag tgt gtt gaa gaa ttt ggt gcc aat gcc 663
108      Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala
109      145      150      155
110      act gtg gaa acc cca gct gct gaa gag aca atg aac acc 702
111      Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
112      160      165      170
113      agc ccg ggg act cct gcc cca gct gct gaa gag aca atg 741
114      Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
115      175      180
116      aac acc agc cca ggg act cct gcc cca gct gct gaa gag 780
117      Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
118      185      190      195
119      aca atg acc acc agc ccg ggg act cct gcc cca gct gct 819
120      Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
121      200      205
122      gaa gag aca atg acc acc agc ccg ggg act cct gcc cca 858
123      Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro
124      210      215      220
125      gct gct gaa gag aca atg acc acc agc ccg ggg act cct 897
126      Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
127      225      230      235
128      gcc tct tct cat tac ctc tca tgc acc atc gta ggg atc 936
129      Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
130      240      245
131      ata gtt cta att gtg ctt ctg att gtg ttt gtt t 970
132      Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
W--> 133      250      255      259
134      gaaagacttc actgtggaag aaattccttc cttacctgaa aggttcaggt 1020
135      aggcgctggc tgaggcggg gggcgctgga cactctctgc cctgcctccc 1070
136      tctgctgtgt tcccacagac agaaacgcct gccctgccc caaaaaaaaaa 1120
137      aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1170
138      aaaaaaaaaa 1180
140 <210> SEQ ID NO: 3
141 <211> LENGTH: 299
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 3
145      Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
146      1      5      10      15
147      Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
148      20      25      30

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149	Arg	Thr	Gln	Asp	Gly	Val	Gly	Asn	His	Thr	Met	Ala	Arg	Ile	Pro
150					35					40					45
151	Lys	Thr	Leu	Lys	Phe	Val	Val	Val	Ile	Val	Ala	Val	Leu	Leu	Pro
152					50					55					60
153	Val	Leu	Ala	Tyr	Ser	Ala	Thr	Thr	Ala	Arg	Gln	Glu	Glu	Val	Pro
154					65					70					75
155	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	Arg	His	Ser	Phe	Lys	Gly
156					80					85					90
157	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg	Ser	Glu	His	Thr	Gly	Ala
158					95					100					105
159	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr	Thr	Asn	Ala	Ser	Asn
160					110					115					120
161	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val	Cys	Lys	Ser	Asp	Gln
162					125					130					135
163	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	Asp	Thr	Val	Cys	Gln
164					140					145					150
165	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn	Ser	Pro	Glu	Met	Cys
166					155					160					165
167	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu	Val	Gln	Val	Ser	Asn
168					170					175					180
169	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	Cys	Val	Glu	Glu	Phe	Gly	Ala
170					185					190					195
171	Asn	Ala	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr
172					200					205					210
173	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr
174					215					220					225
175	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr
176					230					235					240
177	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr
178					245					250					255
179	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr
180					260					265					270
181	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	Tyr	Leu	Ser	Cys	Thr	Ile
182					275					280					285
183	Val	Gly	Ile	Ile	Val	Leu	Ile	Val	Leu	Leu	Ile	Val	Phe	Val	
184					290					295					299

186 <210> SEQ ID NO: 4  
 187 <211> LENGTH: 1180  
 188 <212> TYPE: DNA  
 189 <213> ORGANISM: Homo sapiens  
 190 <220> FEATURE:  
 191 <221> NAME/KEY: CDS  
 192 <222> LOCATION: (73) . . . (969)  
 193 <223> OTHER INFORMATION:  
 194 <220> FEATURE:  
 195 <221> NAME/KEY: sig\_peptide  
 196 <222> LOCATION: (73) . . . (194)  
 197 <223> OTHER INFORMATION:  
 198 <400> SEQUENCE: 4

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199 gctgtgggaa cctctccacg cgcacgaact cagccaacga tttctgatag 50
200 atttttgga gtttgaccag ag atg caa ggg gtg aag gag 90
201 Met Gln Gly Val Lys Glu
202 -40 -35
203 cgc ttc cta ccg tta ggg aac tct ggg gac aga gcg ccc 129
204 Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro
205 -30 -25
206 cgg ccg cct gat ggc cga ggc agg gtg cga ccc agg acc 168
207 Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
208 -20 -15 -10
209 cag gac ggc gtc ggg aac cat acc atg gcc cgg atc ccc 207
210 Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
211 -5 1 5
212 aag acc cta aag ttc gtc gtc gtc atc gtc gcg gtc ctg 246
213 Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu
214 10 15
215 ctg cca gtc cta gct tac tct gcc acc act gcc cgg cag 285
216 Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
217 20 25 30
218 gag gaa gtt ccc cag cag aca gtg gcc cca cag caa cag 324
219 Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln
220 35 40
221 agg cac agc ttc aag ggg gag gag tgt cca gca gga tct 363
222 Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser
223 45 50 55
224 cat aga tca gaa cat act gga gcc tgt aac ccg tgc aca 402
225 His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr
226 60 65 70
227 gag ggt gtg gat tac acc aac gct tcc aac aat gaa cct 441
228 Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro
229 75 80
230 tct tgc ttc cca tgt aca gtt tgt aaa tca gat caa aaa 480
231 Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
232 85 90 95
233 cat aaa agt tcc tgc acc atg acc aga gac aca gtg tgt 519
234 His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
235 100 105
236 cag tgt aaa gaa ggc acc ttc cgg aat gaa aac tcc cca 558
237 Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro
238 110 115 120
239 gag atg tgc cgg aag tgt agc agg tgc cct agt ggg gaa 597
240 Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
241 125 130 135
242 gtc caa gtc agt aat tgt acg tcc tgg gat gat atc cag 636
243 Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln
244 140 145
245 tgt gtt gaa gaa ttt ggt gcc aat gcc act gtg gaa acc 675
246 Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr
247 150 155 160

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/992,964

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Input Set : N:\Crf3\RULE60\09992964.raw  
Output Set: N:\CRF3\01282002\I992964.raw

L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11